

[illegible]

FIGURE 1A

334	CAT	GAG	CCG	CCC	CCA	GAG	343	352	GAG	GAG	ATC	ACT	GGC	361	CCT	GTG	GAT	370	GAG	GAG	ACC	379
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H	E	P	P	P	E	E	P	E	E	I	T	G	P	P	V	D	E	E	E	E	T	T
388	TTC	CTG	AAA	GCT	GCG	GTG	397	406	GGG	AAA	ATG	AAG	GTC	415	ATT	GAG	AAG	424	TTC	CTG	GCT	433
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F	L	K	A	A	V	E	G	K	M	K	V	I	E	K	F	L	A	487	L	A	A	A
442	GAC	GGG	GGG	TCA	GCC	GAC	451	460	TGC	GAC	CAG	TTC	CGT	469	CGG	ACA	GCA	478	CTG	CAC	CGA	487
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D	G	G	S	A	D	T	C	D	Q	F	R	R	T	A	L	H	R	532	L	H	R	R
496	GCT	TCC	CTG	GAA	GGC	CAC	505	514	GAA	ATC	CTG	GAG	AAG	523	CTT	CTA	GAT	532	AAT	GGG	GCC	541
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A	S	L	E	G	H	M	E	I	L	E	K	L	L	D	N	G	A	586	N	G	A	A
550	ACT	GTG	GAC	TTC	CAG	GAT	559	568	CTG	GAC	TGC	ACA	GCC	577	ATG	CAT	TGG	586	GCC	TGC	CGC	595
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T	V	D	F	Q	D	R	L	D	C	T	A	M	H	W	A	C	R	640	A	C	R	R
604	GGG	GGC	CAC	TTA	GAG	GTG	613	622	AAA	CTT	CTG	CAA	AGC	631	CAT	GGA	GCA	640	GAC	ACC	AAT	649
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G	G	H	L	E	V	V	K	L	L	L	Q	S	H	G	A	D	T	N	D	T	N	N

FIGURE 1B

658	667	676	685	694	703
GTG AGG GAT AAG CTG CTG AGC ACC CCG CTG CAC GTG GCA GTC CGG ACA GGG CAG					
V R D K L L S T P L H V A V R T G Q					
712	721	730	739	748	757
GTG GAG ATT GTG GAG CAC TTT CTA TCC CTG GGC CTG GAA ATC AAT GCC AGA GAC					
V E I V E H F L S L G L E I N A R D					
766	775	784	793	802	811
AGG GAA GGG GAT ACT GCC CTG CAT GAC GCT GTG AGG CTC AAC CGC TAC AAA ATC					
R E G D T A L H D A V R L N R Y K I					
820	829	838	847	856	865
ATC AAA CTG CTG CTC CTG CAT GGG GCT GAC ATG ATG ACC AAG AAC CTG GCA GGA					
I K L L L L H G A D M M T K N L A G					
874	883	892	901	910	919
AAG ACC CCG ACG GAC CTG GTG CAG CTC TGG CAG GCT GAT ACC GAT ACC GGC CTG					
K T P T D L L V Q L W Q A D T R H A L					
928	937	946	955	964	973
GAG CAT CCT GAG CCG GGG GCT GAG CAT AAC GGG CTG GAG GGG CCT AAT GAT AGT					
E H P E P G A E H N G L E G P N D S					

FIGURE 1C

FIGURE 1D

982	991	1000	1009	1018	1027
GGG CGA GAG ACC CCT CAG CCT GTG CCA GCC CAG TGA ATG CGT GCC CCA GCC CAG					
G R E T P Q P V P A Q					
1036	1045	1054	1063	1072	1081
CCA GCT ACC CAG CCC CTC TCT GTG TGC AGC CGG AGG GTC CTA AGA ATG GCT CCC					
1090	1099	1108	1117	1126	1135
GGA GCT AAC TGA GGG CCC AGC CTT TTT TCT GCA TGA TCC AGG AGC ACA TAC CAC					
1144	1153				
AAA CTA CCA CAA TAA AAA AGC TG 3'					

FIGURE 1D

1	S	M	E	D	S	E	A	V	Q	R	A	T	A	L	I	E	Q	R	L	A	5578191CD1
1	-	M	E	G	P	E	A	V	Q	R	A	T	E	L	I	E	Q	R	L	A	g9501360
1	-	M	E	G	P	E	A	V	Q	R	A	T	E	L	I	E	Q	R	L	A	g5420272
21	Q	E	E	N	E	K	L	R	G	D	T	R	Q	K	L	P	M	D	L	5578191CD1	
20	Q	E	E	E	T	E	K	L	R	S	A	P	G	K	L	S	M	D	M	g9501360	
20	Q	E	E	E	T	E	K	L	R	S	A	P	G	K	L	S	M	D	M	g5420272	
41	L	V	L	E	D	E	K	H	H	G	A	Q	S	A	A	L	Q	K	V	K	5578191CD1
40	L	V	L	E	E	E	K	R	L	G	V	Q	S	P	A	L	Q	K	V	K	g9501360
40	L	V	L	E	E	E	K	R	L	G	V	Q	S	P	A	L	Q	K	V	K	g5420272
61	G	Q	E	R	V	R	K	T	S	L	D	L	R	R	E	I	I	D	V	G	5578191CD1
60	G	Q	E	R	V	R	K	T	S	L	D	L	R	R	E	I	I	D	V	G	g9501360
60	G	Q	E	R	V	R	K	T	S	L	D	L	R	R	E	I	I	D	V	G	g5420272
81	G	I	Q	N	L	I	E	L	R	K	K	R	K	Q	K	R	D	A	L	5578191CD1	
80	G	I	Q	N	L	I	E	L	R	K	K	R	K	Q	K	R	D	A	L	g9501360	
80	G	I	Q	N	L	I	E	L	R	K	K	R	K	Q	K	R	D	A	L	g5420272	

FIGURE 2A

101	A	A	S	H	E	P	P	P	E	E	I	T	G	P	V	D	E	E	5578191CD1		
100	A	A	A	Q	E	P	P	P	E	E	I	T	G	P	V	N	E	E	g9501360		
100	A	A	A	Q	E	P	P	P	E	E	I	T	G	P	V	N	E	E	g5420272		
121	T	F	L	K	A	A	V	E	G	K	M	K	V	I	E	K	F	L	A	D	5578191CD1
120	T	F	L	K	A	A	V	E	G	K	M	K	V	I	D	K	Y	L	A	D	g9501360
120	T	F	L	K	A	A	V	E	G	K	M	K	V	I	D	K	Y	L	A	D	g5420272
141	G	G	S	A	D	T	C	D	Q	F	R	R	T	A	L	H	R	A	S	L	5578191CD1
140	G	G	S	A	D	T	C	D	E	F	R	R	T	A	L	H	R	A	S	L	g9501360
140	G	G	S	A	D	T	C	D	E	F	R	R	T	A	L	H	R	A	S	L	g5420272
161	E	G	H	M	E	I	L	E	K	L	L	D	N	G	A	T	V	D	F	Q	5578191CD1
160	E	G	H	M	E	I	L	E	K	L	L	E	N	G	A	T	V	D	F	Q	g9501360
160	E	G	H	M	E	I	L	E	K	L	L	E	N	G	A	T	V	D	F	Q	g5420272
181	D	R	L	D	C	T	A	M	H	W	A	C	R	G	G	H	L	E	V	V	5578191CD1
180	D	R	L	D	C	T	A	M	H	W	A	C	R	G	G	H	L	E	V	V	g9501360
180	D	R	L	D	C	T	A	M	H	W	A	C	R	G	G	H	L	E	V	V	g5420272

FIGURE 2B

201	K	L	L	Q	S	H	G	A	D	T	N	V	R	D	K	L	L	S	T	P	5578191CD1	
200	R	L	L	Q	S	R	G	A	D	T	N	V	R	D	K	L	L	S	T	P	g9501360	
200	R	L	L	Q	S	R	G	A	D	T	N	V	R	D	K	L	L	S	T	P	g5420272	
221	L	H	V	A	V	R	T	G	Q	V	E	I	V	E	H	F	L	S	L	G	5578191CD1	
220	L	H	V	A	V	R	T	G	H	V	E	I	V	E	H	F	L	S	L	G	g9501360	
220	L	H	V	A	V	R	T	G	H	V	E	I	V	E	H	F	L	S	L	G	g5420272	
241	L	E	I	N	A	R	D	R	E	G	D	T	A	L	H	D	A	V	R	L	5578191CD1	
240	L	D	I	N	A	K	D	R	E	G	D	S	A	L	H	D	A	V	R	L	g9501360	
240	L	D	I	N	A	K	D	R	E	G	D	S	A	L	H	D	A	V	R	L	g5420272	
261	N	R	Y	K	I	I	K	L	L	L	L	L	H	G	A	D	M	M	T	K	N	5578191CD1
260	N	R	Y	K	I	I	K	L	L	L	L	L	H	G	A	D	M	M	A	K	N	g9501360
260	N	R	Y	K	I	I	K	L	L	L	L	L	H	G	A	D	M	M	A	K	N	g5420272
281	L	A	G	K	T	P	T	D	L	V	Q	L	W	Q	A	D	T	R	H	A	5578191CD1	
280	L	A	G	K	T	P	T	D	L	V	Q	L	W	Q	A	D	T	R	H	A	g9501360	
280	L	A	G	K	T	P	T	D	L	V	Q	L	W	Q	A	D	T	R	H	A	g5420272	

FIGURE 2C

301	L	E	H	P	E	P	G	A	E	H	N	G	L	E	G	P	N	D	S	G	5578191CD1
300	L	E	H	P	E	P	E	S	E	Q	N	G	L	E	R	P	-	G	S	G	g9501360
300	L	E	H	P	E	P	E	S	E	Q	N	G	L	E	R	P	-	G	S	G	g5420272
321	R	E	T	P	Q	P	V	P	A	Q											5578191CD1
319	R	E	T	P	Q	P	I	P	A	Q											g9501360
319	R	E	T	P	Q	P	I	P	A	Q											g5420272

FIGURE 2D

Tissue Distribution

Tissue Category	Clone Count	Found in	Abs Abund	Pct Abund
Cardiovascular System	266190	4/68	4	0.0015
Connective Tissue	144645	0/47	0	0.0000
Digestive System	501101	1/148	1	0.0002
Embryonic Structures	106713	0/21	0	0.0000
Endocrine System	225386	2/53	2	0.0009
Exocrine Glands	254635	0/64	0	0.0000
Genitalia, Female	427284	0/106	0	0.0000
Genitalia, Male	448207	3/114	7	0.0016
Germ Cells	38282	0/5	0	0.0000
Hemic and Immune System	680277	0/159	0	0.0000
Liver	109378	0/35	0	0.0000
Musculoskeletal System	159280	10/47	24	0.0151
Nervous System	955753	4/198	5	0.0005
Pancreas	110207	0/24	0	0.0000
Respiratory System	390086	1/93	2	0.0005
Sense Organs	19256	0/8	0	0.0000
Skin	72292	0/15	0	0.0000
Stomatognathic System	12923	0/10	0	0.0000
Unclassified/Mixed	120926	1/13	1	0.0008
Urinary Tract	279062	3/64	5	0.0018
Totals	5321883	29/1292	51	0.0000

FIGURE 3A

Found in:

Library ID	Clone Count	Library Description	Abs Abund	Pct Abund
MUSCNOT10	3302	muscle, gluteal, mw/clear cell SAR, 43F	11	0.3331
MUSLTDT01	804	muscle, thigh, mw/lipoSAR, 58M	1	0.1244
MUSCNOT02	2541	muscle, psoas, 12M	3	0.1181
MUSLNOT01	3306	muscle, tibial, aw/thrombosis, 41F	2	0.0605
MUSLTDR02	4002	muscle, thigh, mw/lipoSAR, 58M, RP	2	0.0500
MUSCNOT01	2716	muscle, skeletal, mw/malignant hyperthermia	1	0.0368
MUSCDIN06	3043	muscle, thigh, ALS, 74F, NORM	1	0.0329
MUSCDMT01	3137	muscle, calf, mw/gangrene, aw/atherosclerosis	1	0.0319
MUSCDIT06	3192	muscle, skeletal, aw/Krabbe, 11mF	1	0.0313
MUSCNOT07	6491	muscle, forearm, mw/intramuscular hemangioma	1	0.0154

FIGURE 3B

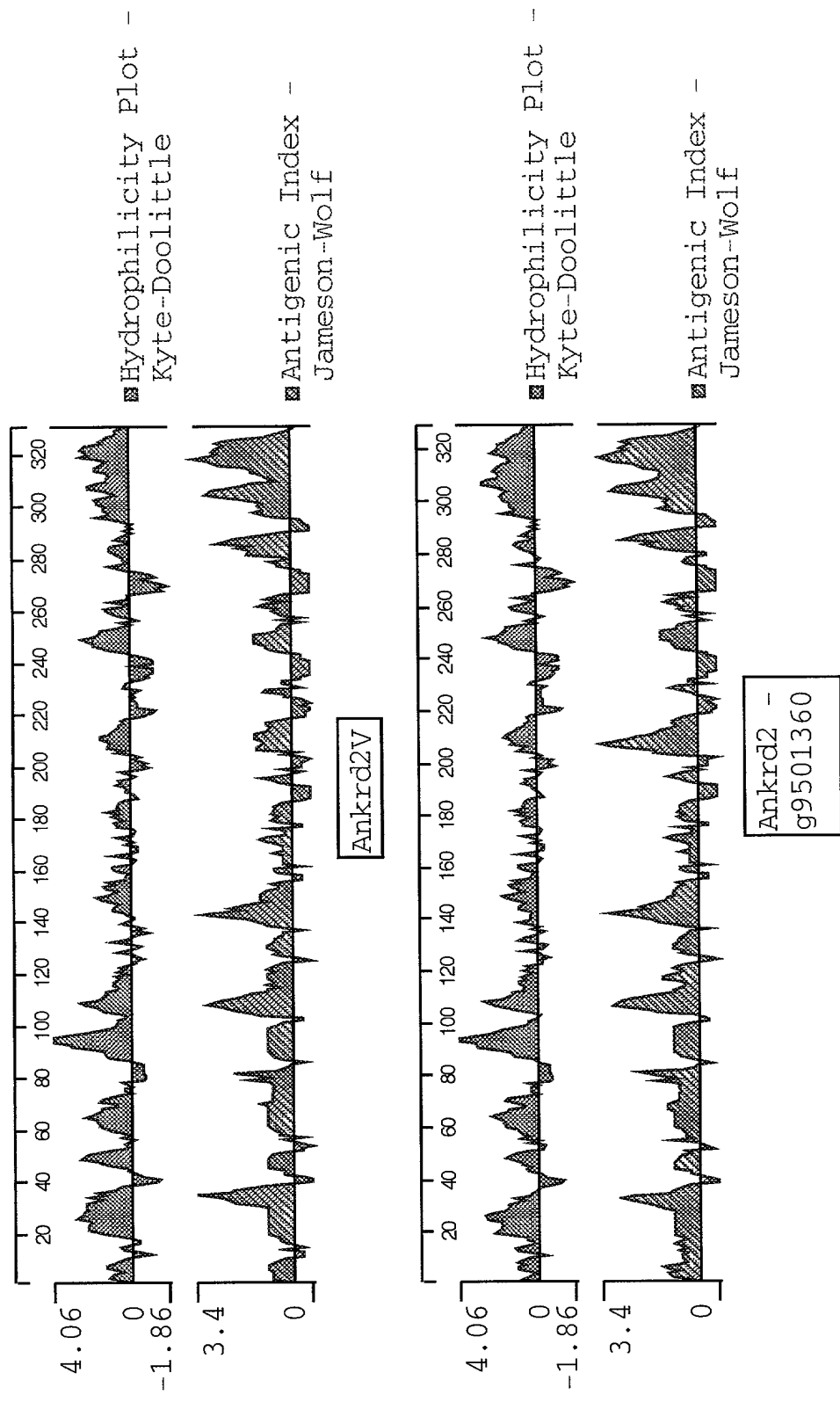


FIGURE 4A

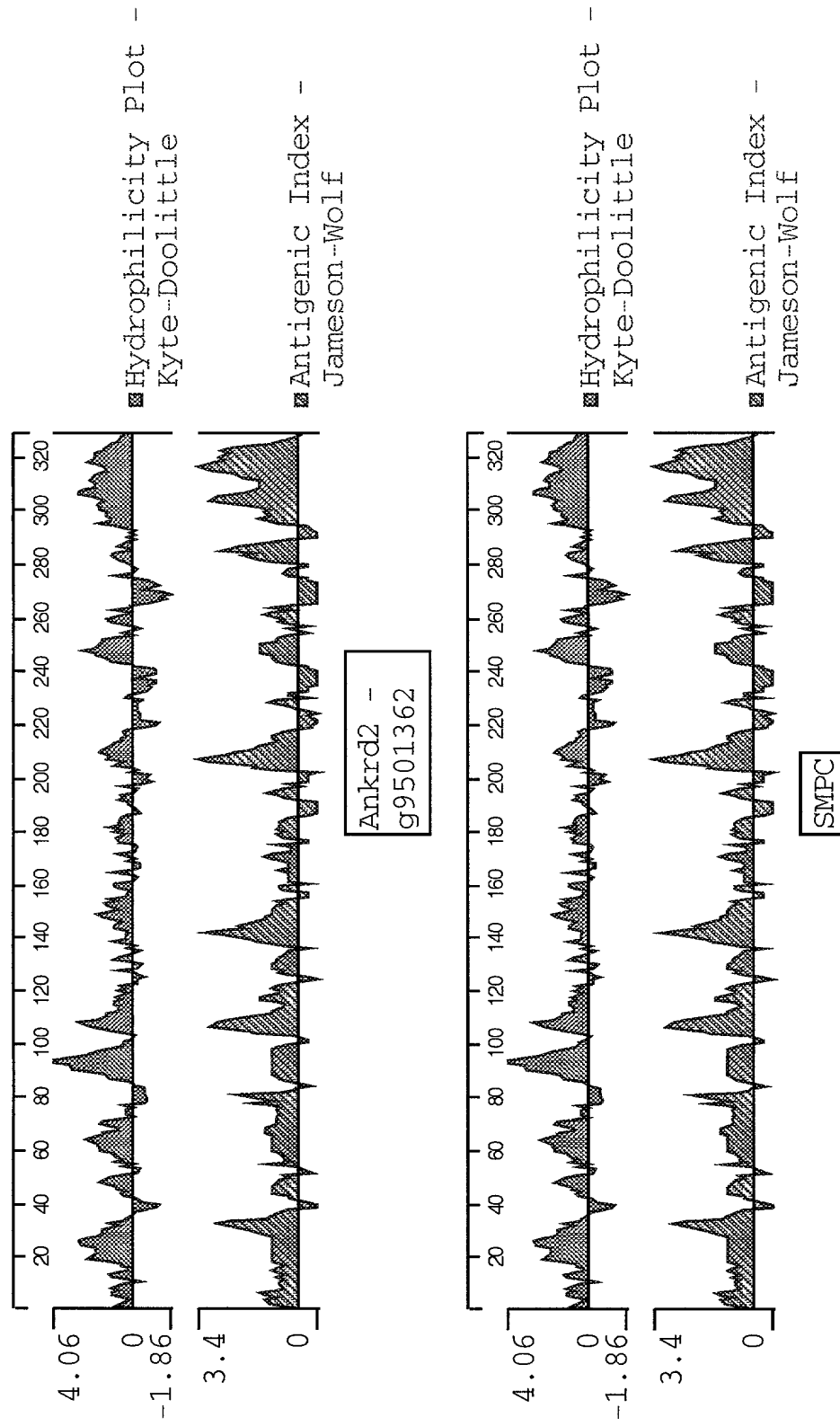


FIGURE 4B